

SEQUENCE LISTING

SEQ ID 1 – NadA from strain 2996, with C-terminus deletion

MKHFPSKVLTTAILATFCSGALAATNDDVKKAATVAIAAAYNNQEINGFKAGETIYDIDEDGTITKKDATAADVEADDF
 KGLGLKKVVTNLTKTVNENKQNVDAKVAAESEIEKLTTKLADTDAALADTDAALDATTNALNKLGENITTFAETKTNIV
 5 KIDEKLEAVADTVDKHAEAFNDIADSLDENTKADEAVKTANEAKQTAETKQNVDAVKAAETAAGKAEAAAGTANTAAD
 KAAEAVAAKVTDIKADIATNKDNIACKANSADVYTREESDSKFVRIDGLNATTEKLDTRLASAEKSIADHDTRLNGLDKTVS
 DLRKETRQGLAEQAALSGLFQPYNVG

SEQ ID 2 – NadA from strain 2996, with C-terminus deletion and leader peptide processed

ATNDDDVKAATVAIAAAYNNQEINGFKAGETIYDIDEDGTITKKDATAADVEADDFKGLGLKKVVTNLTKTVNENKQNV
 10 DAKVAAESEIEKLTTKLADTDAALADTDAALDATTNALNKLGENITTFAEETKTNIVKIDEKLEAVADTVDKHAEAFNDI
 ADSLDENTKADEAVKTANEAKQTAETKQNVDAVKAAETAAGKAEAAAGTANTAADKAEAVAAKVTDIKADIATNKDNI
 AKKANSADVYTREESDSKFVRIDGLNATTEKLDTRLASAEKSIADHDTRLNGLDKTVSDLRKETRQGLAEQAALSGLFQPY
 NVG

SEQ ID 3 – AG741 from MC58 strain

15 VAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAQGAEKTYGNQDSLNTGKLNDKVSRFDFIRQIEVDGQL
 ITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAQGSDDAGGKLTYT
 IDFAAKQNGKIEHLKSPELNVDIAADIKPDGKRHAVISGSVLYNQAEKGSYSLGIFFGKAQEVAEVAKTVNGIRHIG
 LAAKQ

SEQ ID 4 – 936 from MC58 strain with leader peptide processed

20 VSAVIGSAAVGAKSAVDRRTGAQTDDNVMALRIETTARSYLRQNNQTKGYTPQISVVGYNRHLLLGVATEGEKQFVGQ
 IARSEQAAEGVNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQITQKVST
 TVGVQKVITLYQNYVQR

SEQ ID 5 – 953 from MC58 strain with leader peptide processed

25 ATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIR
 FVSTKFNFNGKKLVSDGNLTMHGKTAPVKLKAEKFNQCYQSPMEKTEVCGGDFSTTIDRTKGMDYLNVGMTKSVRIDIQ
 IEAAKQ

SEQ ID 6 – AG287 from MC58 strain

SPDVKSADTLSKPAPVVSEKETEAKEDAPQAGSQGQGAPSAQGSQDMAAVSEENTGNGAVTADNPKNEDEGAQNNDMPQN
 AAGTDSSTPNHTPDPNMLAGNMENQATDAGESSQ PANQPD MANAADGMQGDDPSAGGQNAQNTAAQGANQAGNNQAGSSD
 30 PIPASNPA PANGGSNFGRVDLANGVLIDGPSQNITLTHCKGDSCSGNNFLDEEVQLKSEFEKLSADKISNYKKDGKND
 VGLVADSVQMKGINQYIIIFYKPKPTS FARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNI FAPEGNRYRL
 TYGAEKLPGGSYALRVQGEPAK GEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKVDGIIDSGDDLHMGQTQKF
 KAAIDGNGFKGTWTENGSDVSGKFYGPAGEEVAGKYSYRPTDAEKGGFGVFAKGKEQD
 SEQ ID 7 – 287-953 hybrid

35 MASPDVKSADTLSKPAPVVSEKETEAKEDAPQAGSQGQGAPSAQGSQDMAAVSEENTGNGAAATDKPKNEDEGAQNNDMP
 QNAADTDSLTPNHTPASNMPAGNMENQAPDAGESEQ PANQPD MANTADGMQGDDPSAGGENAGNTAAQGTNQAENNQTAGS
 QNPASSTNPSATNSGGDFGRNVGNVSVIDGPSQNITLTHCKGDSCSGNNFLDEEVQLKSEFEKLSADKISNYKKDGKND
 GKNDKFVGLVADSVQMKGINQYIIIFYKPKPTS FARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNI FAPE
 GNYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSRGRFAAKVDFGSKVDGIIDSGGDGLH
 40 MGTQKFKAIDGNGFKGTWTENGSDVSGKFYGPAGEEVAGKYSYRPTDAEKGGFGVFAKGKEQDGSGGGGATYKVDEYHA
 NARFAIDHFNTSTNVGGFYGLTGSVEFDQAKRDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNNG
 KKLVSVDGNLTMHGKTAPVKLKAEKFNQCYQSPMAKTEVCGGDFSTTIDRTKGVDYLVNVGMTKSVRIDIQIEAAKQ*

SEQ ID 8 – 936-741 hybrid

45 MVSAVIGSAAVGAKSAVDRRTGAQTDDNVMALRIETTARSYLRQNNQTKGYTPQISVVGYNRHLLLGVATEGEKQFVG
 QIARSEQAAEGVNYITVASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQITQKV

TTVGVQKVITLYQNYVQRSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVRKNEKLKLAQGAEKTYGNGLSLN
TGKLNDKVSRFDFIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDFKLP
EGGRATYRGTAFGSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEGSYSLSGI
FGGKAQEVAWSAEVKTVNGIRHIGLAAKQ*

5 **SEQ ID 9 – linker**

GSGGGG

SEQ ID 10 – 741 sequence

CSSGGGGVAADIGAGLADALTAPLDHKDKSLQSLTLDQSVRKNEKLKLAQGAEKTYGNGLSLNTGKLNDKVSRFDFIRQ
IEVDGQLITLESGEFQVYKQSHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDFKLP EGGRATYRGTAFGSDDA
10 GGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEGSYSLSGI FGGKAQEVAWSAEVKTV
NGIRHIGLAAKQ

SEQ ID 11 – 741 sequence

CSSGGGGVAADIGAGLADALTAPLDHKDKSLQSLTLDQSVRKNEKLKLAQGAEKTYGNGLSLNTGKLNDKVSRFDFIRQ
IEVDGQLITLESGEFQIYKQDHSAVVALQIEKINNPDKIDS LINQRSFLVSLGGEHTAFNQLPDGKAEYHGKAFSSDDAG
15 GKLTYTIDFAAKQGNGKIEHLKTPEQNVELAAAELKADEKSHAVILGDTRYGSEEKGTYHLALFGDRAQEIA
GVHEIGIAGKQ

SEQ ID 12 – 741 sequence

CSSGGGGGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEDSIPQNGTLTSLAQGAEKTFKAGDKDNSLNTGKLNDKI
SRFDVQKIEVDGQTITLASGEFQIYKQNHSAVVALQIEKINNPDKTDSSLINQRSFLVSLGGEHTAFNQLPGGKAEYHGK
20 AFSSDDPNGLHYSIDFTKKQGYGRIEHLKTLEQNVELAAAELKADEKSHAVILGDTRYGSEEKGTYHLALFGDRAQEIA
G SATVKIGEVHEIGIAGKQ